

WHAT IS CLAIMED IS:

1. A computer readable medium having stored thereon a nucleic acid sequence as set forth in SEQ ID NO: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto.

2. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence as set forth in SEQ ID NO: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto.

3. The computer system of claim 1, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

4. The computer system of claim 2, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

5. The computer system of claim 1, further comprising an identifier which identifies features in said sequence.

6. A method for comparing a first sequence to a reference sequence wherein said first sequence is a nucleic acid sequence as set forth in SEQ ID Nos: 1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO: 2, and sequences substantially identical thereto comprising:

reading the first sequence and the reference sequence through use of a computer program which compares sequences; and

determining differences between the first sequence and the reference sequence with the computer program.

7. The method of claim 5, wherein determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

8. A method for identifying a feature in a sequence wherein the sequence is as set forth in SEQ ID NO: 1, sequences substantially identical thereto, or a polypeptide sequence of SEQ ID NO: 2, and sequences substantially identical thereto comprising:

reading the sequence through the use of a computer program which identifies features in sequences; and

identifying features in the sequences with the computer program.

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